



# DNA analysis conference in Santa Fe

May 27, 2015

## Record attendance noted for genome and bioinformatics workshop

LOS ALAMOS, N.M., May 27, 2015—This week in Santa Fe, Los Alamos National Laboratory is hosting a DNA sequence analysis and bioinformatics event, the 10th annual [Sequencing, Finishing and Analysis in the Future \(SFAF\) workshop](#).

More than 300 participants from the international scientific community will gather at La Fonda to hear about everything from keynote addresses on the research applications of sequencing data (such as “Evolution and Epidemiology of Anthrax through the Lens of Genome Analysis”) to technical talks that highlight specific strategies such as a comparison of using sequence data from one commercial machine versus another.

“This meeting is more than just a science meeting where scientists share their discoveries and accomplishments,” said Chris Detter, who founded the conference with a committee of researchers from around the world. “From day one it was meant to be a super workshop that has evolved over the past 10 years to bring leaders in the genomics field together with vendors, applications specialists and especially young scientists to discuss how genome sequencing and analysis plays a pivotal role in health, environment and security. The primary focus is to foster communication and collaborations to better enable use of these rapidly evolving technologies,” he said.

When the workshop began in 2006, the human genome project had recently ended and Los Alamos was playing a key role in “finishing” genomes (taking raw sequence data and resolving gaps and repeats to create high quality data) as part of the DOE Joint Genome Institute.

The new conference was an instant success as a venue for participants to share finishing strategies and approaches for gaining the best genomic data. As the conference grew, it began to include forums for industry representatives to hear directly from scientists on what was needed and desired from their sequencing equipment, and it developed a broadened focus that included more about the sequence analysis and bioinformatics challenges associated with using sequence data in research. As sequencing technology has improved—at an exponential pace—researchers now find themselves with virtual mountains of quality data, and analysis has become a major focus of the conference.

“On the international front, this meeting is meant to be inclusive and far reaching,” Detter said. “A goal is to spread this wealth of directly applicable knowledge to as many nations as possible. The SFAF meeting is serving as a nucleus for training and scientific

research for many important regions of the world with the aim of promoting self-sustaining scientific capabilities for positive effects in global health and bio-security,” he noted.

Los Alamos research in genome science has evolved as well over the last decade. After a pivotal role in the early days of the Human Genome Project to a leader in the finishing aspect of the Joint Genome Institute, Los Alamos has also begun to focus its research now on the analysis of sequence data and integrating it with all aspects of biological research. Included in this has been a significant amount of outreach to share sequencing and analysis expertise and software through training programs. Some SFAF participants will stay in New Mexico to attend a bioinformatics training next week on-site at Los Alamos National Laboratory.

Some participants at the bioinformatics workshop will actually be from international genome centers that Los Alamos has helped to establish—in Jordan, the Republic of Georgia, and most recently in Uganda and Gabon. Los Alamos has worked not only to help set up sequencing equipment but also to train personnel to do the sequencing and the analysis, both on site at the locations and also in Los Alamos.

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